

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 10:19:03 : Search time 5267.53 Seconds
(without alignments)
11025.472 Million cell updates/sec

Title: US-09-922-895-3

Perfect score: 3586
Sequence: 1 GGATCCCTACCTTCCCATC.....CTATCAGAGGAGAGTGAA 3586

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	267.6	7.5	549	17	A0838273 HS_4712.A
2	210	5.9	453	10	B6677425 B6677425 7d84b05.x
3	210	5.9	700	17	AG114100 Pan treg1
4	209.6	5.8	450	17	A0035000 CIT-HSP-2
5	206.8	5.8	718	17	A0898001 HS_3135.A
6	203.8	5.7	352	10	AM089016 xd34d02.x

Result No.	Score	Query Match	Length	ID	Description
7	203.2	5.7	656	17	AG132086 Pan treg1
8	202.8	5.7	435	17	A0542219 RPT-11-3
9	202.2	5.6	660	17	AG157820 Pan treg1
10	202.2	5.6	739	17	A0035003 CIT-HSP-2
11	202	5.6	478	9	A1627168 A1627168 ty60a05.x
12	201.8	5.6	513	17	A0418548 RPT-11-2
13	201.6	5.6	782	12	BG743198 602634360
14	201.6	5.6	449	17	A0769842 HS_3170.B
15	201.4	5.6	628	14	BM716611 UI-E-DX1-
16	200.6	5.6	681	17	A0543621 RPT-11-3
17	200.6	5.6	808	12	BG432758 B6432758 602496155
18	200.4	5.6	925	14	BQ433470 AGENCOURT
19	200.2	5.6	852	14	BQ690945 AGENCOURT
20	199.8	5.6	551	17	A0352725 CITB1-E1-
21	199.8	5.6	711	17	A0415030 RPT-11-2
22	199.6	5.6	521	17	AQ237142 RPT-11-65
23	199.6	5.6	15970	17	A0839852 260L13-C5
24	199.4	5.6	518	17	AQ412258 RPT-11-1
25	199.4	5.6	673	14	BM728941 UI-E-E01-
26	199.4	5.6	1024	14	BQ422616 AGENCOURT
27	199.2	5.6	478	17	BM7141 CIT-HSP-201
28	199.2	5.6	933	14	BQ959144 AGENCOURT
29	199	5.5	416	17	AQ140695 HS_3112.A
30	199	5.5	665	17	AG107923 Pan treg1
31	199	5.5	705	17	AG078610 Pan treg1
32	198.8	5.5	500	12	BE779049 601464810
33	198.8	5.5	680	14	BM990843 UI-H-D10-
34	198.6	5.5	805	17	AQ739187 HS_5382-B
35	198.6	5.5	843	14	BQ421400 AGENCOURT
36	198.4	5.5	489	9	A1160786 A1160786 qc75609.x
37	198.4	5.5	573	17	BA7427 CIT978SK-A-
38	198.4	5.5	674	17	AG123283 Pan treg1
39	198.2	5.5	466	14	BQ573431 UI-H-E21-
40	198.2	5.5	700	17	AG013777 Homo sapi
41	198.2	5.5	718	17	AG178110 Pan treg1
42	198.2	5.5	798	12	BG535971 602564142
43	198	5.5	879	14	BQ708582 AGENCOURT
44	198	5.5	2205	11	AF318346 Homo sapi
45	197.8	5.5	457	9	A1628859 A1628859 ty17d08.x

ALIGNMENTS

RESULT 1
A0838273/c 549 bp DNA linear GSS 30-AUG-1999
DEFINITION HS_4712_A2_H05_SPEE CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-4712 Col-10 Row-O, DNA sequence.
ACCESSION A0838273
VERSION A0838273.1 GI:5808147
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 549)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL MEDLINE
COMMENT Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Oudeen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu

Plate: 4712 row: 0 column: 10
Seq primer: T7
Class: BAC ends
High quality sequence stop: 549.

FEATURES

Location/Qualifiers
1..549

source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=4712 Col=10 Row=0"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 162 a 115 c 95 g 172 t 5 others
ORIGIN

Query Match 7.5%; Score 267.6; DB 17; Length 549;
Best Local Similarity 84.4%; Pred. No. 3.1e-31;
Matches 335; Conservative 0; Mismatches 57; Indels 5; Gaps 3;

QY 924 ATTTACGATTACCTTATGTTTCCCAAAATGTAAGGCCATT-TTGAAGCCTAATTC 982

DB 396 ATTTAAAGAAAGCTATACAGTATCAAAATAGTAACGAGCCATTGAGAGCTTATTC 337

QY 983 AAACCTTCA--CTATTTGTATCTAAGTATTCACCTTGATTGAGACTGGTAGACAG 1040

DB 336 GATCATCTCCATCATATGTAATGTAGTATCCATCATGATGAGACTGGTAGACAGG 277

QY 1041 TGAAGACCATATCAGTTTATTTTATTTTATTTATTTATTTATTTATTTT 1100

DB 276 TGAAGACCATATCAGTTTATTTTATTTTATTTTATTTATTTATTTATTTCT 219

QY 1101 TTTGAGATGAGTCTGGCTGTCCGCCAGGCTGAGTGACAGCGGGTGATCAGATTCACT 1160

DB 218 TTGAGATGAGTCTGGCTGTCCGCCAGGCTGAGTGACAGCGGGTGATCAGATTCACT 159

QY 1161 GCAGCCCAACCTTTGAGCTCAAGGATTCCTCCACCTCAGCCCCCAAGTAGTGGGA 1220

DB 158 GCAGCCCAACCTTTGAGCTCAAGGATTCCTCCACCTCAGCCCCCAAGTAGTGGGA 99

QY 1221 CCACAGCTATGCGCCACCATGCGCTGCTAATTTCTTTTGTAGAGTAGATCTC 1280

DB 98 CCACAGCTATGCGCCACCATGCGCTGCTAATTTCTTTTGTAGAGTAGATCTC 39

QY 1281 ACTATATTGTCAGAGCTGTCTTGAAATTCCTGGGCTC 1317

DB 38 ACTATATTGTCAGAGGATGCTGAATTCGGCGGATC 2

RESULT 2 453 bp mRNA linear EST 08-SEP-2000
BE677425
LOCUS 7d84b05.x1 lupski.dorsal.root.ganglion Homo sapiens cDNA clone

DEFINITION IMAGE:3279633.3; similar to contains Alu repetitive element

ACCESSION BE677425

VERSION BE677425

KEYWORDS BE677425.1 GI:10037894

SOURCE EST.

ORGANISM Homo sapiens

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 453)

NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Journal National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Dr. James Lupski

CDNA Library Preparation: Lupski Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: infoimage.lnl.gov
Seq primer: -40UP from G1bco
High quality sequence stop: 406.

FEATURES

source

1..453
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3279633"
/clone_lib="Lupski.dorsal.root.ganglion"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/note="Vector: PCWV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTCTAGATCGGAGCGCGCCCTT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

BASE COUNT 117 a 109 c 98 g 129 t
ORIGIN

Query Match 5.9%; Score 210; DB 10; Length 453;

Best Local Similarity 76.3%; Pred. No. 1.8e-22;

Matches 258; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1064 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1123

DB 3 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 62

QY 1124 CCAGGCTGAGTGACAGCGCGTGAATCAGTTCAGCTCAGCTTCCAGCTCA 1183

DB 63 CCAGGCTGAGTGACAGCGCGTGAATCAGTTCAGCTCAGCTTCCAGCTCA 122

QY 1184 AGGATTCCTCCACCTCAGCGCCCAAGTAGTGGGACACAGTATGCGCCCATGGC 1243

DB 123 AGGATTCCTCCACCTCAGCGCCCAAGTAGTGGGACACAGTATGCGCCCATGGC 182

QY 1244 TGCTTAATTTCTAATTTTGTAGAGATGATGATGATGATGATGATGATGATGAT 1303

DB 183 TGCTTAATTTCTAATTTTGTAGAGATGATGATGATGATGATGATGATGATGAT 242

QY 1304 GAATTCCTGGGCTCAGGTGAGCTCCACCTGGGCTCCCAAGTAGTGGGATTCAGGCG 1363

DB 243 CAATCTCTGGGCTCAGGTGAGCTCCACCTGGGCTCCCAAGTAGTGGGATTCAGGCG 302

QY 1364 ATGAGCCCAAGTCCCTCCCATATGAGATTTCTGTC 1401

DB 303 GTGAGCCACTGCACTCAGTGGGAGCCCTTCTAATTC 340

RESULT 3 700 bp DNA linear GSS 03-NOV-2001
AG114100/c

LOCUS AG114100

DEFINITION Pan troglodytes DNA, clone: PTB-120022.R, genomic survey sequence.

ACCESSION AG114100

VERSION AG114100.1 GI:16734619

KEYWORDS GSS.

SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male

BAC library clone:PTB-120022.R.

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of library PTB

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 700)
AUTHORS	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Tokoi,Y., Watanabe,H. and Sakaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 17-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 220-0045, Japan (E-mail:chimbegsc@riken.go.jp, URL:http://nsp.gsc.riken.go.jp/, Tel.:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PMB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
COMMENT	PRIMERS Sequencing: M13Rev LIBRARY Vector : pRS145 R.Site 1 : SacI R.Site 2 : SacI Location/Qualifiers 1..700 /organism="Pan troglodytes" /db_xref="taxon:9598" /clone="PMB-120022.R" /sex="male" /cell_type="lymphoblast" /clone_id="PMB Chimpanzee Male BAC Library"
BASE COUNT	200 a 167 c 176 g 157 t
ORIGIN	
Query Match	5.9% Score 210; DB 17; Length 700;
Best Local Similarity	81.9%; Pred.No.1,5e-22;
Matches 254; Conservative	0; Mismatches 55; Indels 1; Gaps 1;
OY 1079	TTATTTATTATTTAATTTATTTTGTAGATGAGCTGGCTGCAGCCAGCGTGAGTGC 1138
Db 494	TTATTTATTATTTATTTTA-TTTTGAACAGACTCTCTCTGTGCCCGGTGAGTGC 436
OY 1139	AGCGCGTGATCACAGTTCACTGCAGCCTCAACCTTAGCGTCAAAGGATTTGCCACC 1198
Db 435	TGTGATGTGATCTCGCTACGTGAGCCTCTAATCTCTGAGCTCAAGTATCTCCCACC 376
OY 1199	TCAGCCCCCAAGTAGTGGGAGCACAGCATATGCCACACATGGCTGATTTCTTAT 1258
Db 375	TCAGCCTCCCAAGTAGTGGGAGCTACAGGACAGTCCACCATGCTGGATGATTTGTTA 316
OY 1259	TTTTTTAGAGATATGAGATCTACATATTTGTCAGCGCTGGTGAATTCCTGGGCTCA 1318
Db 315	ACTTTTGAAGACACAAGTTTACATATGTTGCCAGGTTGGTCTTGAATCTCTGGCTCA 256
OY 1319	GGTGAGCTCCACACCTGGGCTCCCAAGAATACTGGGATTAACAGGATGAGCCAGTCC 1378
Db 255	AGTGATCTCTCGCTCCTCAGCCTCCCAAGAGTGTGGATTAACAGGGGTGACACAGCAC 196
OY 1379	CTGCCCATAT 1388
Db 195	CAGCCAGGAT 186
RESULT 4	
LOCUS	AO035000 450 bp DNA linear GSS 11-JUL-1998
DEFINITION	CIT-HSP-2333P5.TF CIT-HSP Homo sapiens genomic clone 2333P5, DNA sequence.
ACCESSION	AO035000
VERSION	AO035000.1 GI:3301174
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 450) Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,...

[illegible]

ORGANISM	Homo sapiens Euryotola; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 718)
REFERENCE	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzel,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.hnsc.washington.edu Plate: 3135 Row: O Column: 14 Seq primer: T7 Class: BAC ends High quality sequence stop: 718.
FEATURES	Location/Qualifiers 1..718 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_plate=3135 COL=14 Row=O /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male" /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT	149 a 157 c 122 g 287 t 3 others
ORIGIN	
Query Match	5.8%; Score 206.8; DB 17; Length 718;
Best Local Similarity	74.0%; Pred. No. 4.5e-22;
Matches 262; Conservative	0; Mismatches 92; Indels 0; Gaps 0;
Oy	1056 GTTTTAAATTTTTTAATTATTTAATTTATTTATTTATTTATTTAGATGAGTCT 1115
Dd	194 GTTTATAGATTATTTATTTATTTATTTATTTATTTATTTATTTCTGACAGATCC 253
Oy	1116 GCCTGTGCCAGCGGTGAGTGACGGCGGTGATCACACTTCACAGCACTTC 1175
Dd	254 CACTCTTCCAGGCATAGTAGAGGGCGCATCGCGCTACAGCAACTTGGCTCC 313
Oy	1176 TAGGCTCAAGGATTCCTCCACCCTCAGCCCCCAAAGTAGTGGACACAGCTATGCGCC 1235
Dd	314 TGGAATTCAGAGCCCTCTCTGCTGCTCAGGCTCCCGAGTAGCTGATTTACAGGCGTGACAC 373
Oy	1236 ACCATGCGCGGTAAATTTCTTATTTTTTTGTAGAGTAGATCATCTATATTGCCAGG 1295
Dd	374 ACCATGCGCTGGCTAAATTTTGTATTTTGGTAGACATGAGGCTTACCGTGTGGCCAGG 433
Oy	1296 CTGTCTTGAATTCCTGGGCTCAGGTGAGACCTCCACACCTGGGCTCCCAAATAGTGGGA 1355
Dd	434 CTGGTCTCAAACTCTCGACCTCAAGTGAATCCCGCGCTTGGCCTCCCAAATGCTGGGA 493
Oy	1356 TTACAGGCGTAGGCAAGGTCCCCTGCGCCCATATGAGATTTCTGTCTGATCC 1409
Dd	494 TTACAGGTGTGAGCATCATGCTGGCCCTGTTTATAGATTTCTTTATGATGCC 547
RESULT 6	
AW089016/c	
LOCUS	AW089016 352 bp mRNA linear EST 15-OCT-1999
DEFINITION	x634402.x1 NCL CGAP Ov23 Homo sapiens cDNA clone IMAGE:259551 3'
'	similar to contains Alu repetitive element.;contains element HGR
'	repetitive element ;, mRNA sequence.
ACCESSION	AW089016
VERSION	AW089016.1 GI:6044851

KEYWORDS						
SOURCE	EST.	human.				
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)				
REFERENCE AUTHORS	Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: www.bio.lnl.nl.gov/bdnp/image/image.html Seq primer: -400P from Gldco High quality sequence stop: 321.					
JOURNAL COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaaps.r@email.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.					
TITLE						
FEATURES	location/Qualifiers					
SOURCE	1..352					
	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
	/clone="IMAGE:2595651"					
	/clone_lib="NCI CGAP_Ov23"					
	/tissue_type="tumor, 5 pooled (see description)"					
	/lab_host="DH10B"					
	/note="Organ: ovary; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"					
BASE COUNT	115 a	81 c	82 g	74 t		
ORIGIN						
Query Match	5.7%;	Score 203.8;	DB 10;	Length 352;		
Best Local Similarity	76.5%;	Pred. No. 1.8e-21;				
Matches 250;	Conservative 0;	Mismatches 77;	Indels 0;	Gaps 0;		
OY 1072	TTTTTAATTATTTATTTATTTATTTAGATGGATGTGGCTGGCCAGGCT	1131				
I	I I I I I I I I I I I I I I I I I I I	I	I I I I I I I I I I			
Db 337	TATGATGATGAATGATGATGATTTATTTATTTTGAGAGAACTGTGCCTGTCAACCAGGCT	278				
OY 1132	GGAGTCACGCCGCTGATCACAGTTCACTGCAGCCTCAACTTCTTAGCTCAAGGATTC	1191				
Db 277	GGAGTCAGATGGCACGATCTCGGCTCACTACACTCTGCCCTTGGGGTTCAAAGTATTC	218				
OY 1192	TCCCACATCAGCCCCCAAAGTATGTGGGACACAGTATGGGCGAACAATGGCTGGCTAAT	1251				
Ddb 217	TCCCACCTCAGCTCTCTAGTACGTGGGATTTACAGCATGGGCGACGACCTCGGTGAAT	158				
OY 1252	TTCTATATTTTGTAGAGATAGATCTCAGTATATTTTCCAGGCTGCTTGAATTCCT	1311				
Db 157	TTTTGTATTTTATAGTAGAATGGSGTTTCCACATTTTACCAAGCTGGTCTTGATTAAGT	98				
OY 1312	GGGCTCAGGTGAGCTCCACACTGGGCTCCCAAAAGTACTGGGATTTACAGCATGAGCCA	1371				
Db 97	GACCTCAGGTGATCCACCACTTGGCTCCCAAAAGTCTGGGATTTACAGCATGAGCCA	38				
OY 1372	AGGTCCCTGCCCAATGAGATTTCT	1398				
Db 37	CTGTGCCCGGCTCATTTTTTTTTT	11				

[illegible]

DEFINITION	RPCI-11-36J1J3.TU RPCI-11 Homo sapiens genomic clone RPCI-11-36J1J3 , DNA sequence.
ACCESSION	AQ542219
VERSION	AQ542219.1 GI:4872675
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 435) Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter ,J.C. Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building Unpublished (1997)
JOURNAL	Other GSSs: RPCI-11-36J1J3.TV
COMMENT	Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbeet@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (http://www.fgrr.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: SP6 Class: BAC ends.
FEATURES	Location/Qualifiers 1..435 /organism="Homo sapiens" /db_xref="GDB:7638468" /db_xref="taxon:9606" /clone="RPCI-11-36J1J3" /clone_id="RPCI-11" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT	87 a 110 c 101 g 137 t
ORIGIN	
Query Match	5.7%: Score 202.8; DB 17; Length 435;
Best Local Similarity	74.9%: Pred. No.2.3e-21;
Matches 268; Conservative	0; Mismatches 87; Indels 3; Gaps 1;
OY 1039	GGTGAAGCAATATCAGCTTTTAATTTTTTAATTTAATTATTTATTTATTTAT 1098
Dd 41	GGTAGACTCTCCACGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTAT 97
OY 1099	TTTTTGAGATGAGTCGTGGCTGTGCGCCAGCGCTGAGTCGACGGCGTATCACAGTTCA 1158
Dd 98	TTTGGACAGAGTCCTGCTGTGTGCCCCAGCGCTGCGTGCAGTGCATGATCTCAGCTCA 157
OY 1159	CTGACGCTCAACCTTCAAGGCTCAAGGAGTTTCCCACCTCAGCCCCCAAGTAGTTGG 1218
Dd 158	CTGCACCTCCACCCTCCCGGGTTCAGCAAAATTTCTCGCTCAGCTCCCAAGTAGCTGG 217
OY 1219	GACCAACGTAATGGCCACCAATGCTCGCTAAATTTCTAATTTTGTAGAGATAGATC 1278
Dd 218	GACCAACAGTGTGGCCACCAACATGCTCGCTAATTTTTCATTTTATAGTAGAGACGGGTT 277
OY 1279	TCACTATAATGTCCAGCGCTGCTTGAATTCCTGGGCTCAGAGTGAGCTCCACCTGGGC 1338
Dd 278	TCACTATTTGTGGCCAGCGCTGTTCAAATCTCCTCAGCTCAGAGTGATTCACCCACCTTGGC 337
OY 1339	CTCCCAAGTACTGGGATTAACAGCATAGCCCAAGTCCCTGCGCCATATGAGATTTT 1396
Dd 338	CTCCCAAGTCTGGGATTAACAGCTGATGATGACGCCCCACACTTTCATCGTGGCTTTT 395

RESULT 9
LOCUS AG157820 660 bp DNA linear GSS 09-JAN-2002
DEFINITION Pan troglodytes DNA, clone: RP43-022N18.TJ, genomic survey sequence.
ACCESSION AG157820
VERSION AG157820.1 GI:16687498
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphocytes DNA, clone_lib=RPCT-43 Chimpanzee Male BAC Library Clone:RP43-022N18.TJ.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Torokl,Y., Matanabe,H. and Sakaki,Y. BAC end sequences of library RPCT-43 unpublished 2 (bases 1 to 660)
JOURNAL Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Torokl,Y., Matanabe,H. and Sakaki,Y. Direct Submission Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimbeseqsc.riken.go.jp, URL:http://bgp.gsc.riken.go.jp/, Tel.:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library RPCT-43 This BAC clones was generated during the R&D process and may have higher chance of clone tracking errors. PRIMERS
COMMENT Sequencing: TJ
LIBRARY Vector : pBACe3.6 R.Site 1 : EcoRI R.Site 2 : EcoRI. Location/Qualifiers 1..660 /organism="Pan troglodytes" /db_xref="taxon:9598" /clone="RP43-022N18.TJ" /sex="male" /cell_type="lymphocytes" /clone_lib="RPCT-43 Chimpanzee Male BAC Library"
FEATURES source
BASE COUNT 166 a 154 c 135 g 205 t
ORIGIN
Query Match 5.6%; Score 202.2; DB 17; Length 660; Best Local Similarity 74.3%; Pred. No. 2.3e-21;
Matches 255; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
OY 1056 GTTTTAATTTTTTAAATTATAATTTAATTTAATTTAATTTTGAGATGAGACT 1115 DbB 59 GTTAATTAATTAATTAATTAACCTATTTTAATTTAATTTAATTTTGACAAGACTTCG 118
OY 1116 GGCTGTGCCCAAGCGGTGAGTGACAGCGCATGATCAGATTCAGCCCAACCTTC 1175 Db 119 TTCTGTGGCCAGCGGTGAGTGACATGAGCGGCATCTCGGCTCACAGAACCTCGCTTCC 178
OY 1176 TAGGCTCAAAGAATTCCTCCCACCTACGCCCCCCAAGTAGTGGGAACACAGTATGCGCC 1235 Db 179 CGGGTTCAGAGTGTATCTCACACCCTCAGCCTCCGAGTAGCTGGAGCTCAGCGGCTGCC 238
OY 1236 ACCATGCGGTGATTTCTTAAATTTTGTGAGATAGGATCAGTATATGTCGAGG 1295
Db 239 AACATGCCCCGGCTAATTTTGTATTAGTAGAACAAGGTTTACTATGTTGGCCAGG 298
OY 1296 CTGGTCTGAANTTCCTGGGCTCAGGTGAGACCTCCACACTGGCGCTCCCAAGTATGGGA 1355
Db 299 CTGGCTCGAANTTCCTGACCTCAATGATGATGAGCCCGCCTCAGCCTCCCAAGTGTGGGA 358
OY 1356 TTACAGGCATGAGCCAAGTCCCTGCCCAATATGAGATTTTCT 1398

Db	359	TTATAGCATGAGCCACGTGTGCCGGCCCATTTAATTGTATA	401
RESULT 10			
AQ035003/C		AQ035003	739 bp DNA linear GSS 11-JUL-1998
LOCUS		CIT-HSP-2333P7.FR CIT-HSP Homo sapiens genomic clone 2333P7, DNA	
DEFINITION		sequence.	
ACCESSION		AQ035003	
VERSION		AQ035003.1	GI:3501177
KEYWORDS		GSS.	
SOURCE		human.	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE		1 (bases 1 to 739)	
AUTHORS		Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.	
		Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)	
JOURNAL		Unpublished (1998)	
COMMENT		Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (Info@resgen.com). BAC end search page: http://www.tigr.org/tcdb/humgen/bac_end_search/Bac_end_search.html . Seq primer: M13 Reverse Class: BAC ends.	
FEATURES		Location/Qualifiers	
source		1..739	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
		/clone_id="2333P7"	
		/clone_1id="CIT-HSP"	
		/sex="Male"	
		/cell_type="Sperm"	
		/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII."	
BASE COUNT		246 a 147 c 175 g 171 t	
ORIGIN			
Query Match		5.6%; Score 202.2; DB 17; Length 739; Best Local Similarity 74.3%; Pred. No. 2.e-21;	
Matches 255; Conservative 0; Mismatches 88; Indels 0; Gaps 0;			
QY	1059	TTTAATTTTTTAATTTAAATTTAATTTAATTTAATTTAATTTTGAGATGAGCTGTGC	1118
DB	555	TTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTTGGATGGAGTCATTC	496
QY	1119	TGTCCCGCAGGCTGAGTCGACGGCGATGATCACAGTTCACTCGACGCTCAACTTTAG	1178
DB	495	TATTTCCCAAGCTGAGTCGACGTGATGATTCGCTTCACGACAACCTCTCTCCAG	436
QY	1179	GCTCAAGGATCTCCACCTCAGCCCCCACCAGTAGTTGAGACACACAGATGAGCCAC	1238
DB	435	GTTCAAAGCATCTCTCTCCCTCAGCTCCCCCAGTAGCTGGATTACAGCAGCAGCCAC	376
QY	1239	ATGCTGCGCTAATTTCTATTATTTTGTAGAGATAGATCTCATATTTGTCCAGGCTG	1298
DB	375	ATGCCAGCTAATTTTGAATTTTAATGAGAGACGGGTTTCACCATGTTGCCAGGCTG	316
QY	1299	GTCCTGAATCTCTGGGCTCAGCTGAGCCCTCCACCTAGGGCTCCCAAGTACTGGGATTA	1358
DB	315	GTCCTGAATCTCTGACCTCAGGTGATCCACCGCCTTGCCCTACCAAGAATGCTGAGATTA	256

[illegible]

DB	241	CTCAGGTGCTCCACCGGCTCGGCTCCCAAGTCTAGGATTACAGGCATGACCACT	300
OY	1375	TCGCCGCAATATAGATTTTCTGTCTGTATGCCATGACAGCTAGTATCAAGACTTG	1434
DB	301	CATCAGCGCTATTCACCTTTTCTGATTTGATTTGACTTATGATGACGATCATATAGCTG	360
OY	1435	GC 1436	
DB	361	AC 362	
RESULT 12			
LOCUS	A0418548	513 bp	DNA linear
DEFINITION	RPCT-11-204J7.TV	RPCT-11	Homo sapiens genomic clone RPCT-11-204J7, DNA sequence.
ACCESSION	A0418548		
KEYWORDS	A0418548.1	GI:4476272	GSS.
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 513) Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.		
TITLE	Use of BAC End Sequences from Library RPCT-11 for Sequence-Ready Map Building		
JOURNAL	Unpublished (1997)		
COMMENT	Other_GSSs: RPCT-11-204J7.TV Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are derived from the human BAC library RPCT-11. For BAC library availability, please contact Pieter de Jong (pieter@edjong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet. cs (http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html). Seq primer: T7 Class: BAC ends.		
FEATURES	Location/Qualifiers		
SOURCE	1..513 /organism="Homo sapiens" /db_xref="GDB:7578174" /db_xref="taxon:9606" /clone="RPCT-11-204J7" /clone_lib="RPCT-11" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCT11 Human Male BAC library"		
BASE COUNT	104 a 127 c 94 g 188 t		
ORIGIN			
Query Match	5.6%;	Score 201.8;	DB 17; Length 513;
Best Local Similarity	74.5%;	Pred. No. 3e-21;	
Matches 254;	Conservative 0;	Mismatches 87;	Indels 0; Gaps 0;
OY	1044	AAACCATATCAGGCTTTTATATTTTAAATTTTAAATTTATTTATTTATTTATTTT	1103
DB	9	ATACCTATACCTTATCTTATCTTTCTTTTCTTTTATTTCTTTTCTTTTCTTTGACTTTT	68
OY	1104	GAGATGGAGTGGCGTGGCGGACGAGCTGAGTGCAGGGCGGATGATCAGATTCACATGCA	1163
DB	69	GAAATGGAGTCTACATGCTACCCAGGCTGAGTGCAGTGTGTGATCTCTGGCTCATGTGCA	128
OY	1164	GCCTAACCTTTAGAGCTCAAGGATTTCTCCACACGACACCCCAAGTATTTGGGACCA	1223

[illegible]

